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Sequence Listing was accepted.
If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).
Reviewer: markspencer
Timestamp: [year=2009; month=8; day=7; hr=14; min=1; sec=32; ms=695; ]
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Application No: 10583785   Version No: 4.0

Input Set:

Output Set:

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             Finished:  2009-07-31 15:25:18.514
              Elapsed:  0 hr(s) 0 min(s) 15 sec(s) 76 ms
       Total Warnings:  22
         Total Errors:  0
 No. of SeqIDs Defined:  40
   Actual SeqID Count:  40
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W   213   Artificial or Unknown found in <213> in SEQ ID (13)

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W   213   Artificial or Unknown found in <213> in SEQ ID (35)

W   213   Artificial or Unknown found in <213> in SEQ ID (36)

W   213   Artificial or Unknown found in <213> in SEQ ID (37)

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       Input Set:


       Output Set:



         Started:  2009-07-31 15:25:03.438
        Finished:  2009-07-31 15:25:18.514
         Elapsed:  0 hr(s) 0 min(s) 15 sec(s) 76 ms
  Total Warnings:  22
    Total Errors:  0
No. of SeqIDs Defined:  40
Actual SeqID Count:  40
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Error code   Error Description

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SEQUENCE LISTING

<110> SEEGER, WERNER
      GUNTHER, ANDREAS
      RUPPERT, CLEMENS
      MARKART, PHILIPP
      MAGDOLEN, VIKTOR
      WEAVER, TIMOTHY E.

<120> NOVEL CHIMERIC PLASMINOGEN ACTIVATORS AND THEIR PHARMACEUTICAL
      USE

<130> VJP-1050-US

<140> 10583785
<141> 2009-07-31

<150> PCT/EP2003/014542
<151> 2003-12-18

<160> 40

<170> PatentIn version 3.5

<210> 1
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<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(1143)
<223> Coding sequence of the surfactant protein B precursor

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atg gct gag tca cac ctg ctg cag tgg ctg ctg ctg ctg ctg ccc acg   48
Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Leu Pro Thr
1   5   10   15

ctc tgt ggc cca ggc act gct gcc tgg acc acc tca tcc ttg gcc tgt   96
Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys
            20   25   30

gcc cag ggc cct gag ttc tgg tgc caa agc ctg gag caa gca ttg cag   144
Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln
        35   40   45

tgc aga gcc cta ggg cat tgc cta cag gaa gtc tgg gga cat gtg gga   192
Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly
    50   55   60

gcc gat gac cta tgc caa gag tgt gag gac atc gtc cac atc ctt aac   240
Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn
65   70   75   80

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aag atg gcc aag gag gcc att ttc cag gac acg atg agg aag ttc ctg          288
Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Thr Met Arg Lys Phe Leu
            85                  90                  95

gag cag gag tgc aac gtc ctc ccc ttg aag ctg ctc atg ccc cag tgc          336
Glu Gln Glu Cys Asn Val Leu Pro Leu Lys Leu Leu Met Pro Gln Cys
            100                 105                 110

aac caa gtg ctt gac gac tac ttc ccc ctg gtc atc gac tac ttc cag          384
Asn Gln Val Leu Asp Asp Tyr Phe Pro Leu Val Ile Asp Tyr Phe Gln
        115                 120                 125

aac cag act gac tca aac ggc atc tgt atg cac ctg ggc ctg tgc aaa          432
Asn Gln Thr Asp Ser Asn Gly Ile Cys Met His Leu Gly Leu Cys Lys
        130                 135                 140

tcc cgg cag cca gag cca gag cag gag cca ggg atg tca gac ccc ctg          480
Ser Arg Gln Pro Glu Pro Glu Gln Glu Pro Gly Met Ser Asp Pro Leu
145                 150                 155                 160

ccc aaa cct ctg cgg gac cct ctg cca gac cct ctg ctg gac aag ctc          528
Pro Lys Pro Leu Arg Asp Pro Leu Pro Asp Pro Leu Leu Asp Lys Leu
                165                 170                 175

gtc ctc cct gtg ctg ccc ggg gcc ctc cag gcg agg cct ggg cct cac          576
Val Leu Pro Val Leu Pro Gly Ala Leu Gln Ala Arg Pro Gly Pro His
                180                 185                 190

aca cag gat ctc tcc gag cag caa ttc ccc att cct ctc ccc tat tgc          624
Thr Gln Asp Leu Ser Glu Gln Gln Phe Pro Ile Pro Leu Pro Tyr Cys
            195                 200                 205

tgg ctc tgc agg gct ctg atc aag cgg atc caa gcc atg att ccc aag          672
Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro Lys
            210                 215                 220

ggt gcg cta gct gtg gca gtg gcc cag gtg tgc cgc gtg gta cct ctg          720
Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val Pro Leu
225                 230                 235                 240

gtg gcg ggc ggc atc tgc cag tgc ctg gct gag cgc tac tcc gtc atc          768
Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser Val Ile
                245                 250                 255

ctg ctc gac acg ctg ctg ggc cgc atg ctg ccc cag ctg gtc tgc cgc          816
Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val Cys Arg
                260                 265                 270

ctc gtc ctc cgg tgc tcc atg gat gac agc gct ggc cca agg tcg ccg          864
Leu Val Leu Arg Cys Ser Met Asp Asp Ser Ala Gly Pro Arg Ser Pro
            275                 280                 285

aca gga gaa tgg ctg ccg cga gac tct gag tgc cac ctc tgc atg tcc          912
Thr Gly Glu Trp Leu Pro Arg Asp Ser Glu Cys His Leu Cys Met Ser
        290                 295                 300

gtg acc acc cag gcc ggg aac agc agc gag cag gcc ata cca cag gca          960
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Val Thr Thr Gln Ala Gly Asn Ser Ser Glu Gln Ala Ile Pro Gln Ala
305                 310             315                 320


atg ctc cag gcc tgt gtt ggc tcc tgg ctg gac agg gaa aag tgc aag      1008
Met Leu Gln Ala Cys Val Gly Ser Trp Leu Asp Arg Glu Lys Cys Lys
                325             330             335


caa ttt gtg gag cag cac acg ccc cag ctg ctg acc ctg gtg ccc agg      1056
Gln Phe Val Glu Gln His Thr Pro Gln Leu Leu Thr Leu Val Pro Arg
                340             345             350


ggc tgg gat gcc cac acc acc tgc cag gcc ctc ggg gtg tgt ggg acc      1104
Gly Trp Asp Ala His Thr Thr Cys Gln Ala Leu Gly Val Cys Gly Thr
            355             360             365


atg tcc agc cct ctc cag tgt atc cac agc ccc gac ctt                  1143
Met Ser Ser Pro Leu Gln Cys Ile His Ser Pro Asp Leu
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<210> 2
<211> 837
<212> DNA
<213> Homo sapiens



<220>
<221> CDS
<222> (1)..(837)
<223> Coding sequence of the surfactant protein B precursor lacking
      the C-terminal propeptide


<400> 2
atg gct gag tca cac ctg ctg cag tgg ctg ctg ctg ctg ctg ccc acg       48
Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Leu Pro Thr
1               5               10              15


ctc tgt ggc cca ggc act gct gcc tgg acc acc tca tcc ttg gcc tgt       96
Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys
            20              25              30


gcc cag ggc cct gag ttc tgg tgc caa agc ctg gag caa gca ttg cag      144
Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln
        35              40              45


tgc aga gcc cta ggg cat tgc cta cag gaa gtc tgg gga cat gtg gga      192
Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly
    50              55              60


gcc gat gac cta tgc caa gag tgt gag gac atc gtc cac atc ctt aac      240
Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn
65              70              75              80


aag atg gcc aag gag gcc att ttc cag gac acg atg agg aag ttc ctg      288
Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Thr Met Arg Lys Phe Leu
                85              90              95
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```
gag cag gag tgc aac gtc ctc ccc ttg aag ctg ctc atg ccc cag tgc        336
Glu Gln Glu Cys Asn Val Leu Pro Leu Lys Leu Leu Met Pro Gln Cys
            100                 105                 110


aac caa gtg ctt gac gac tac ttc ccc ctg gtc atc gac tac ttc cag        384
Asn Gln Val Leu Asp Asp Tyr Phe Pro Leu Val Ile Asp Tyr Phe Gln
        115                 120                 125


aac cag act gac tca aac ggc atc tgt atg cac ctg ggc ctg tgc aaa        432
Asn Gln Thr Asp Ser Asn Gly Ile Cys Met His Leu Gly Leu Cys Lys
    130                 135                 140


tcc cgg cag cca gag cca gag cag gag cca ggg atg tca gac ccc ctg        480
Ser Arg Gln Pro Glu Pro Glu Gln Glu Pro Gly Met Ser Asp Pro Leu
145                 150                 155                 160


ccc aaa cct ctg cgg gac cct ctg cca gac cct ctg ctg gac aag ctc        528
Pro Lys Pro Leu Arg Asp Pro Leu Pro Asp Pro Leu Leu Asp Lys Leu
                165                 170                 175


gtc ctc cct gtg ctg ccc ggg gcc ctc cag gcg agg cct ggg cct cac        576
Val Leu Pro Val Leu Pro Gly Ala Leu Gln Ala Arg Pro Gly Pro His
                180                 185                 190


aca cag gat ctc tcc gag cag caa ttc ccc att cct ctc ccc tat tgc        624
Thr Gln Asp Leu Ser Glu Gln Gln Phe Pro Ile Pro Leu Pro Tyr Cys
        195                 200                 205


tgg ctc tgc agg gct ctg atc aag cgg atc caa gcc atg att ccc aag        672
Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro Lys
    210                 215                 220


ggt gcg cta gct gtg gca gtg gcc cag gtg tgc cgc gtg gta cct ctg        720
Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val Pro Leu
225                 230                 235                 240


gtg gcg ggc ggc atc tgc cag tgc ctg gct gag cgc tac tcc gtc atc        768
Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser Val Ile
                245                 250                 255


ctg ctc gac acg ctg ctg ggc cgc atg ctg ccc cag ctg gtc tgc cgc        816
Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val Cys Arg
                260                 265                 270


ctc gtc ctc cgg tgc tcc atg                                            837
Leu Val Leu Arg Cys Ser Met
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<212> DNA
<213> Homo sapiens


<220>
<221> CDS
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<222> (1)..(237)
<223> Coding sequence of the mature surfactant protein B

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Phe Pro Ile Pro Leu Pro Tyr Cys Trp Leu Cys Arg Ala Leu Ile Lys
1   5   10   15

cgg atc caa gcc atg att ccc aag ggt gcg cta gct gtg gca gtg gcc   96
Arg Ile Gln Ala Met Ile Pro Lys Gly Ala Leu Ala Val Ala Val Ala
            20   25   30

cag gtg tgc cgc gtg gta cct ctg gtg gcg ggc ggc atc tgc cag tgc   144
Gln Val Cys Arg Val Val Pro Leu Val Ala Gly Gly Ile Cys Gln Cys
        35   40   45

ctg gct gag cgc tac tcc gtc atc ctg ctc gac acg ctg ctg ggc cgc   192
Leu Ala Glu Arg Tyr Ser Val Ile Leu Leu Asp Thr Leu Leu Gly Arg
    50   55   60

atg ctg ccc cag ctg gtc tgc cgc ctc gtc ctc cgg tgc tcc atg   237
Met Leu Pro Gln Leu Val Cys Arg Leu Val Leu Arg Cys Ser Met
65   70   75

<210> 4
<211> 1293
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(1293)
<223> Coding sequence of the single-chain urokinase-plasminogen
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1   5   10   15

gac tcc aaa ggc agc aat gaa ctt cat caa gtt cca tcg aac tgt gac   96
Asp Ser Lys Gly Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp
            20   25   30

tgt cta aat gga gga aca tgt gtg tcc aac aag tac ttc tcc aac att   144
Cys Leu Asn Gly Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile
        35   40   45

cac tgg tgc aac tgc cca aag aaa ttc gga ggg cag cac tgt gaa ata   192
His Trp Cys Asn Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile
    50   55   60

gat aag tca aaa acc tgc tat gag ggg aat ggt cac ttt tac cga gga   240
Asp Lys Ser Lys Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly
65   70   75   80

```
aag gcc agc act gac acc atg ggc cgg ccc tgc ctg ccc tgg aac tct          288
Lys Ala Ser Thr Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser
                85                  90                  95


gcc act gtc ctt cag caa acg tac cat gcc cac aga tct gat gct ctt          336
Ala Thr Val Leu Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu
                100                 105                 110


cag ctg ggc ctg ggg aaa cat aat tac tgc agg aac cca gac aac cgg          384
Gln Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg
        115                 120                 125


agg cga ccc tgg tgc tat gtg cag gtg ggc cta aag ccg ctt gtc caa          432
Arg Arg Pro Trp Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln
        130                 135                 140


gag tgc atg gtg cat gac tgc gca gat gga aaa aag ccc tcc tct cct          480
Glu Cys Met Val His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro
145                 150                 155                 160


cca gaa gaa tta aaa ttt cag tgt ggc caa aag act ctg agg ccc cgc          528
Pro Glu Glu Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg
                165                 170                 175


ttt aag att att ggg gga gaa ttc acc acc atc gag aac cag ccc tgg          576
Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp
                180                 185                 190


ttt gcg gcc atc tac agg agg cac cgg ggg ggc tct gtc acc tac gtg          624
Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val
        195                 200                 205


tgt gga ggc agc ctc atc agc cct tgc tgg gtg atc agc gcc aca cac          672
Cys Gly Gly Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His
        210                 215                 220


tgc ttc att gat tac cca aag aag gag gac tac atc gtc tac ctg ggt          720
Cys Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly
225                 230                 235                 240


cgc tca agg ctt aac tcc aac acg caa ggg gag atg aag ttt gag gtg          768
Arg Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val
                245                 250                 255


gaa aac ctc atc cta cac aag gac tac agc gct gac acg ctt gct cac          816
Glu Asn Leu Ile Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His
                260                 265                 270


cac aac gac att gcc ttg ctg aag atc cgt tcc aag gag ggc agg tgt          864
His Asn Asp Ile Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys
        275                 280                 285


gcg cag cca tcc cgg act ata cag acc atc tgc ctg ccc tcg atg tat          912
Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr
        290                 295                 300
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aac gat ccc cag ttt ggc aca agc tgt gag atc act ggc ttt gga aaa          960
Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys
305             310             315             320


gag aat tct acc gac tat ctc tat ccg gag cag ctg aaa atg act gtt          1008
Glu Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val
            325             330             335


gtg aag ctg att tcc cac cgg gag tgt cag cag ccc cac tac tac ggc          1056
Val Lys Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly
            340             345             350


tct gaa gtc acc acc aaa atg ctg tgt gct gct gac cca cag tgg aaa          1104
Ser Glu Val Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys
            355             360             365


aca gat tcc tgc cag gga gac tca ggg gga ccc ctc gtc tgt tcc ctc          1152
Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu
            370             375             380


caa ggc cgc atg act ttg act gga att gtg agc tgg ggc cgt gga tgt          1200
Gln Gly Arg Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys
385             390             395             400


gcc ctg aag gac aag cca ggc gtc tac acg aga gtc tca cac ttc tta          1248
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